AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application. Please amend the claims as follows.

1. (Original) A method for identifying a compound having the ability to modulate virus propagation in a host cell comprising the steps of:

(a) generating a three-dimensional model of a protein required for viability of a virus, or a portion thereof;

(b) generating a three-dimensional model of a potential modulator compound of interest; and

(c) determining at least one atomic interaction between the potential modulator compound and the protein, or a portion thereof, as defined by the three-dimensional models of (a) and (b).

2-6. (Canceled).

7. (Canceled).

8. (Original) A method for identifying a compound having the ability to modulate orthopox virus propagation in a host cell comprising the steps of:

(a) generating a three-dimensional model of an I7L protein, or a portion thereof,

(b) generating a three-dimensional model of a potential modulator compound of interest; and

(c) determining at least one atomic interaction between the potential modulator compound and the I7L, or a portion thereof, as defined by the three-dimensional models of (a) and (b).

9-81. (Canceled).

82. (New) The method of claim 1, wherein the virus is an orthopox virus.

83. (New) The method of claim 82, wherein the protein is the vaccinia virus I7L protein.

84. (New) The method of claim 1, wherein steps (a) (b) and (c) further comprise:

(a) generating a three-dimensional computer model of the protein, or a portion thereof;

(b) generating a three-dimensional computer model of the potential modulator compound of interest;

(c1) using a computer to dock the three-dimensional model of the potential modulator compound with the model of the protein or a portion thereof; and

(c2) quantifying at least one atomic interaction between the potential modulator compound and the protein, or a portion thereof.

85. (New) The method of claim 84, further comprising:

(d) modifying the computer model of the potential modulator compound of interest; and

(e) evaluating how modifying the computer model of the potential modulator compound changes at least one atomic interaction between of the model of the potential modulator compound and the model of the protein, or portion thereof.

86. (New) The method of claim 85, wherein the step of modifying the computer model of the potential modulator compound comprises:

(i) searching a library of molecular structures for molecular fragments that can be linked to the potential modulator compound, wherein a molecular fragment comprises at least one atom; and

(ii) linking a fragment to the potential modulator compound to generate a modified computer model of the compound.

87. (New) The method of claim 8, wherein the model of I7L protein, or a portion thereof, comprises the atomic coordinates as defined in Table 2.

88. (New) The method of claim 8, wherein the method of generating the computer model comprises aligning the structure of the I7L protein, or a portion thereof, with a second cysteine protease, or a portion thereof.

89. (New) The method of claim 88, wherein the second cysteine protease is ubiquitin-like protein 1 (ULP1) protease, or a portion thereof.

90. (New) The method of claim 89, wherein the amino acids used to align the structure of the I7L protein, or a portion thereof, with the ULP1, or a portion thereof, comprise His241, Asp248, and Cys328 of the I7L protein and His514, Cys580 and Trp448 of ULP1.

91. (New) The method of claim 8, wherein steps (a), (b) and (c) further comprise:

(a) generating a three-dimensional computer model of the I7L protein, or a portion thereof;

(b) generating a three-dimensional computer model of the potential modulator compound;

(c1) using a computer to dock the three-dimensional model of the potential modulator compound with the model of the I7L protein, or a portion thereof; and

(c2) quantifying at least one atomic interaction between the potential modulator compound and the I7L protein, or a portion thereof.

92. (New) The method of claim 91, further comprising the steps of:

(d) modifying the computer model of the potential modulator compound; and

(e) evaluating how modifying the computer model of the potential modulator compound changes the atomic interactions between of the model of the potential modulator compound and the model of the I7L protein, or portion thereof.

93. (New) The method of claim 92, wherein the step of modifying the computer model of the potential modulator compound comprises:

(i) searching a library of molecular structures for molecular fragments that can be linked to the potential modulator compound, wherein a molecular fragment comprises at least one atom; and

(ii) linking a fragment to the potential modulator compound to generate a modified computer model of the compound.

94. (New) The method of claim 8, wherein the I7L protein, or a portion thereof, comprises a ligand binding domain.

95. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises an atomic interaction between the compound and the catalytic cysteine.

96. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least one atomic interaction between the compound and at least one of amino acids Cys328, His241, Asp248, or Asp258 of the I7L protein.

97. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least one atomic interaction between the compound and at least one of Leu324, Trp242, Gln322, Gly329, Leu323, Ser240, Trp168, Asp194, Asn171, Ser173, Gln 322, Met195, Ser326, Glu327, Leu239, Leu177, Asn199, Met169, Phe236, Ile203,or Met233 of the I7L protein.

98. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises Cys(N), wherein position N corresponds to the catalytic cysteine of the I7L.

99. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least one atomic interaction between the compound and at least one of His(N-87), Asp(N-80), or Asp(N-70), wherein position N corresponds to the catalytic cysteine of the I7L.

100. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least one atomic interaction between the compound and at least one of Trp(N-86), Gln(N-6), Leu(N-4), Gly(N+1), Leu(N-5), Ser(N-88), Trp(N-160), Asp(N-134), Asn(N-157), Ser(N-155), Met(N-133), Ser(N-2), Glu(N-1), Leu(N-89), Leu(N-151), Asn(N-129), Met(N-159), Phe(N-92), Ile(N-125), or Met(N-95),wherein position N corresponds to the catalytic cysteine of the I7L.

101. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least one atomic interaction between the compound and at least one of a wild-type or altered amino acid in the I7L protein corresponding to positions 168, 169, 171, 173, 177, 194, 195, 199, 203, 233, 236, 239, 240, 241, 242, 248, 258, 322, 323, 324, 326, 327, 328, or 329 of the wild-type I7L protein.

102. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least one atomic interaction selected from the group consisting of charge, electrostatic, hydrogen bond, and hydrophobic.

103. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or portion thereof, comprises at least two hydrogen bond atomic interactions, at least two hydrophobic atomic interactions, and at least one of a charge or electrostatic interaction.

104. (New) The method of claim 8, wherein the atomic interaction between a potential modulator compound and the I7L protein, or a portion thereof, comprises at least three hydrogen bond atomic interactions, at least three hydrophobic atomic interactions, and at least one of a charge or electrostatic interaction.

105. (New) The method of claim 8, wherein the potential modulator compound is evaluated for its interaction with a modified I7L protein, or portion thereof, comprising amino acid substitutions, deletions and insertions of the I7L.

106. (New) The method of claim 8, wherein the orthopox virus comprises smallpox virus, vaccinia virus, monkeypox virus, mulluscipox virus, cowpox virus, camelpox virus, variola major virus, variola minor virus, ectromelia virus, sheeppox virus, lumpy skin virus, Yaba-like virus, swinepox virus, rabbit fibroma virus, myxoma virus, fowlpox virus, or canarypox virus.